#### STIC-Biot ch/ChemLib



From: Sent: To:

Subject:

Hamud, Fozia

Wednesday, January 22, 2003 3:59 PM STIC-Biotech/ChemLib

sequence search for 09/714,792

Please, search SEQ ID NO: 4 of 09/714, 792 against commercial and interference data bases. Thanks.

Fozia Hamud Patent Examiner Art Unit 1647 Crystal-Mall-One, Room 10Bo5 Mail Box CM1-10B19 308-8891

Point of Contact P. Sheppard Telephone number: (703) 308-4499

Searcher:
Phone:
Location:
Date Picked Up:
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Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
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Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
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01-JUL-1993 (Rel. 26, Last sequence update)
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Interleukin-5 receptor alpha chain precursor
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BINDS TO IL-5.

C -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BE CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED ALTERNATIVE SPLICING.

C -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHIL C -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

C -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.

C -!- DATABASE: NAME-PROW; NOTE-CD guide CDw125 entry;

C -!- DATABASE: NAME-PROW; NOTE-CD guide CDw125, htm".
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InterPro; IPR003532; Hemtopoptn_S_F2.
InterPro; IPR003532; Hemtopoptn_S_F2; 1.
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"A human high affinity interleukin-5
an IL5-specific alpha chain and a bet
for GM-CSF.";
Cell 66:1175-1184(1991).
-!- FUNCTION: THIS IS THE RECEPTOR FC
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Receptor; Transmembrane; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:6017; IL5RA.
                    Similarity
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, Plaetinck
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26.6%;
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                                                                        INTERLEUKIN-5 RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . 
  70;
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Mismatches
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                    310.5;
No. 3.2
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                                       DВ
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  156;
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  Indels
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                                                                                                                                                                                                          "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."; Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).

C -! FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
C ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY STATIARITY).

C GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).

C SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, CLIBA-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).

C TESTIS. STOMACH, BRAIM, SKIN, AND COLON. BUT NOT SKELETAL MUSCLE.

TESTIS. STOMACH, BRAIM, SKIN, AND COLON. BUT NOT SKELETAL MUSCLE.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor
13RA-1) (Interleukin-13 binding protein) (NR4).
IL13RA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                         or send an email
                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009030;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Willson T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilton D.J., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=96133964; PubMed=8552669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
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                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
    MGI:105052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKICHLWIKLFP 373
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                      S80963;
                                                                             requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KCVTILHKGFSASVRTILQ----NDHSLLASSWASAELH-APPGSPGTSIVNLTCT
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                      AAB50695.1;
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                                                           to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.-G.,
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Rodentia;
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Sciurognathi; Muridae;
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                                                                                                            There are no restrictions ong as its content is in
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1131_HUMAN STANDARD; PRT; 427 AA.
P78552; Q99656; O95646;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor
13RA-1) (CD213al antigen).
IL13RA1 OR IL13RA OR IL13R.
        TISSUE-Carcinoma;
MEDLINE-97165986; PubMed-9013879;
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                 SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=9606;
                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRYFSHFDDQQDKKIAPET------HRKEELPLDEKICLQVGS----QCSANESEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGCLYTFLIST-TFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECT
                                                                                                                                                                                                                                                                                                                                                            SIGKEONSTEYTTMLLTIPV-FVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                              SESDRNMEGTSCFQLPGVLADAVYTVRVRVKTNKLCF-----DDNKLWSDWSEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPDPP-HIKHLLKNGALLVQWKNPQN-FRSRCLTYEVEVNNTQTDRHNILEVEEDKCQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLVKKC--ISPPEGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLYYWYSSLE
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; IPR003532; Hemtopoptn_S_F2.
PS01356; HEMATOPO_REC_S_F2; 1.
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1 25 POTENTIAL.
Laurent P.,
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                                                                                                 Chordata;
Primates;
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25.8%;
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BY SIMILARITY.
N-LINKED (GLCN)
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CYTOPLASMIC
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                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Lupker
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.4e-17
J., Caput D., Vita
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THE PROPERTY OF A COLUMN AND COLU
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Gauchat J.F.M., Schlagenha
Jeannin P., Alouani S., El.
Eugster H.P., Bonnefoy J.Y
Submitted (JAN-1997) to th
                                              DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
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-!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.

--- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.

--- SUBCELLULAR LOCATION: Type I membrane protein.

--- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER, SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.

--- SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.

--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

--- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.inho.
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y10659; CAA71669.1; -. EMBL; Y09328; CAA70508.1; -. EMBL; U62858; AAB37127.1; -. EMBL; U81379; AAD00510.3; -.
    CARBOHYD
                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of IL4R alpha
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                           CHAIN
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Submitted (SEP-1999)
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                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
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Aman M.J., Tayebi
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002996; CR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:5974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         ; IPR003532; PS01356; HE
                                                                                                                                                                                                                                                                                                                    Transmembrane;
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271:29265-29270(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlagenhauf E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human IL-13R alphal chain and reconstitution with the functional IL-4/IL-13 receptor complex.";
                                                                                                                                                                                                                                                                                                             32; Hemtopoptn_S_F2.
   HEMATOPO_REC_S_F2; 1.
mbrane; Glycoprotein; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                IL13RA1.
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e EMBL/GenBank/DDBJ databases
                                                                                                         EXTRACELLULAR (POTENTIAL)
POTENTIAL)
CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL
BY SIMILARITY.
BY SIMILARITY
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Notarangelo L.D.,
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                                                                                                                                                                                                                                               (POTENTIAL).
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01-JUN-1994
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                      between
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                                                                                                                                                                                                                                    Tanaka M.,
                                                                                                                                                                                                                                                    STRAIN=White leghorn; MEDLINE=93075121; Pub!
                                                                                                                                                                                                                                                                                                                                                                       Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prolactin
                                                                                                                                                                                                              Tanaka M., Maeda K., Okubo T., Nakash
Double antenna structure of chicken
                                                                                                                                                                                                                                                                                                 SEQUENCE
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Local
  ween the European
                                                                                                                                                      cDNA sequence. chem. Biophys. FUNCTION: THIS
                                                                            PROLACTIN.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
SIMILARITY: CONTAINS
                                      SWISS-PROT entry is copyright.
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                                                                          COCATION: Type I membrane protein.

BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAIN
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1. 36, Past annotation (
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Neognathae; Galliformes; Phasianidae; Phasiani
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Bioinformatics and the EMBL outstation -
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InterPro; IPR003961; FN_III.
InterPro; IPR003928; Hemtopoptn_L_F1.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
IL5R_MOUSE
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HSSP; P16471; 1BP3.
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                                                                                                                                                                                                                                                                                      TTFGCTSSSDTEIKVN--PPQDFE---IVDPG---
                                              VLGVLSSLICLIMSWTMVLKGYRMITFMLP
                                                               PFGFI - - LILVIFVTGLLLRKPNTYPKMIP
                                                                                                                    DPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ
                                                                                                                                       LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR----EDDTTLVTATVEN
                                                                                                                                                                           DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
                                                                                                                                                                                             WSEWSSERHILIPSGQSPPEKPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE
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                                                                                 QTQYKMFSLNPGKKYI-----IQIHCKPDHHGSWSEWSSENYIQIPNDFRVKDMI-VWI
                                                                                                 ET-YTLKTTNETROLCFVVRSKVNIYCSDD--GIWSEWSDKQCWE-GEDLSKKTLLRFWL
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                                                                                                                                                                                                                                                                                                                  Similarity
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STANDARD;
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26.4%;
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.
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Pred. No. 5
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BY SIMILARITY.
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EMBO J. 9
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ILSRA OR ILDK.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; Metazoa; Rodentia; Motaria; Rodentia;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91092260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takatsu
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                                                                    84
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                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN IS COMMON TO THE IL-3, IL-5 AND SUBCELLULAR LOCATION: Type I membrane TISSUE SPECIFICITY: EXPRESSED ON EOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDS TO IL-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ON B-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                             ; D90205; BAA14231.1;
S12357; S12357.
MGI:96558; I15ra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                    VTPLHEGFAASVRTILK - - - SSHTTLASSWVSAEL - KAPPGSPGTSVTNLTCTTHTVVSS
                                                                                         GFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
                                                                                                                PPVNFTIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES---KC
                                                                                                                                    PPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKD
                      HTHLRPYQVSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPR
 -YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:4367-4374(1990).
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                     ; Transmembrane; (17 18 415 18 339 361 362 415 117 193 193 32 179 193 241 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning
                                            -WQY-LLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNIGCRFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tominaga
                                                                                                                                                                                                            415
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2265612;
ga A., Mita S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and expression
                                                                                                                                                                                                            46989
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24.6%;
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                                                                                                                                                              70;
                                                                                                                                                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (PC
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N-LINKED
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Pred.
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                                                                                                                                                                                                            A4326D2922571C08
                                                                                                                                                             Mismatches
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                                                                                                                                                                         247;
No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       (GLCNAC
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151;
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(POTENTIAL).
(POTENTIAL).
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            DOMAIN
TRANSMEM
                                                                                                                                        EMBL;
HSSP;
                                                                                                                                                               EMBL;
                                             SIGNAL
                                                                                        InterPro; IPR003961; F
InterPro; IPR003528; H
Pfam; PF00041; fn3; 4.
                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the companies of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                      Pitts G.R., You S.K., Submitted (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                             TISSUE-Ovary;
Pitts G.R., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97057891; PubMed-8902221; Zhou J.F., Zadworny D., Guemene D., Kuhn. "Molecular cloning, tissue distribution,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meleagris gallopavo (Common turkey)
Eukaryota; Metazoa; Chordata; Crani
Archosauria; Aves; Neognathae; Gall
 DOMAIN
                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                      prolactin receptor during various
gallopavo.";
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                                                                                                                           InterPro;
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TISSUE-Kidney;
                                    CHAIN
                                                           Receptor;
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                                                                                                                                        L76587; AAB01544.1; -. U22947; AAA75038.1; -. U22924; AAA75039.1; -. P16471; 1BP3.
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                                                                                                                                                                                                                                                                                                                                                                                                           Reprod. 55:1081-1090(1996).
                                                                                  SM00060;
                                                                    PS01352; HEMATOPO_REC_L_F1;
                                                                                                                 IPR002996; CR1A.
IPR003961; FN_III.
                                                        Transmembrane;
 24
24
439
460
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 23
831
438
459
831
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Neognathae; Galliformes; Meleagrididae; Meleag
                                                                                                                                                                                                                                                                                                                                      , Foster D.N., el Halawani M.E.;
to the EMBL/GenBank/DDBJ databases.
'S A RECEPTOR FOR THE ANTERIOR PITUITARY
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                                                                                                     Hemtopoptn_L_F1.
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PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(TPRLR).
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MBL outstation -
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RESULT 8
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P31785;
01-JUL-1993
01-JUL-1993
15-JUN-2002
Cytokine rec
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         Science [2]
                               Munakata
"Cloning
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                                                    SEQUENCE FROM N.A., MEDLINE=92335883; PTakeshita T., Asao
                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Conser
                     H., Nakamura M., Si
y of the gamma chain
257:379-382(1992).
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1993 (Rel.
2002 (Rel.
e receptor
tor gamma c
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Metazoa; Chordata; C
-···horia; Primates; (
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N.A
                                                       Asao H.,
                                                                                                                                                      11. 26, Created)
11. 26, Last sequence update)
11. 26, Last annotation update)
11. 41, Last annotation precursor
12 cor common gamma chain precursor
13 chain) (IL-2R gamma chain) (Pf
                                                                                                                                                                                                                                   STANDARD;
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                                                      Ohtani K., Ishii N.,
                                Sugamura
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Pred. No. 6.7e
53; Mismatches
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BY SIMILARITY.
N-LINKED (GLCNAC.
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                                                                                                                Craniata; V
Catarrhini;
                                                                                                                                                                                                                                   PRT;
                                                                              SEQUENCE
                                 K.;
human
                                                                                                                                                             precursor (Gamma-C)
chain) (P64) (CD132
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                                                                                                                            Vertebrata;
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V TYPE-III
V TYPE-III
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.7e-12;
                                 IL-2
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                                                                                                                 Hominidae;
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                                                       Kumaki S.,
                                receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 831;
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                                                                                                                            Euteleostomi;
                                                                                                                 Homo
                                                        Tanaka
                                                                                                                                                             (Interleukin-
antigen).
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   Kondo M., Takeshir...

Kondo M., Takeshir...

Arai K.-1., Sugamura K.;

"Sharing of the interleukin-2 (IL-2) re
"sharing of IL-2 and IL-4.";

receptors for IL-2 and IL-4.";

Science 262:1874-1877(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure ...

[8]
VARIANTS XSCID PHE-115; CYS-240 AND 1LE--
VARIANTS ASSET PHE-115; CYS-240 AND 1LE--
VARIANTS ASSET A., Certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modelling.
Structure
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J. B:
                                                  MEDLINE=94300093; PubMed=8027558; Ishii N., Asao H., Kimura Y., Takeshita T., Konno T., Maeda M., Uchiyama T., Sugamura K "Impaliment of ligand binding and growth si receptor gamma-chains in patients with X-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94130970; PubMed-829
Disanto J.P., Dautry-Varsat
de Saint Basile G.;
                                                                                                                                                                                                                                                                                            "Detection of three nonsense mutations the interleukin-2 receptor gamma chain differently affect the mRNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked severe combined immunodeficiency disease result in the loss of high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
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Kondo M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The interleukin-2 receptor gamma chain maps in X-linked severe combined immunodeficiency, Hum. Mol. Genet. 2:1099-1104(1993).
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                                                                                                                                                                                                                                                                                                                                                                                       Markiewicz S., Subtil A., de Saint Basile G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WARIANT XSCID LYS-68 MEDLINE=94375038; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE MODELING OF 57-248.
MEDLINE-95111955; PubMed-7529123;
Bamborough P., Hedgecock C.J., Richar
"The interleukin-2 and interleukin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Interleukin-2 receptor gamma interleukin-7 receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION AS MEDLINE=94090316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-4 receptor.";
Science 262:1880-1883(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION AS A 1 MEDLINE=94090317; Puk Russell S.M., Kkegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Willard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                            immunodeficiency.
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Immunol.
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                                                                                                                                                                                                             XSCID
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153:1310-1317(1994).
                                                                                                                                                                                                             HIS-162
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PubMed=8266077;
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                                                     nding and growth signaling of mutant IL-2 patients with X-linked severe combined
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Miyajima A.
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SCIDX1."
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Paul W.E
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Jones A.M., Clark
Cant A., Kinnon C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                           "Atypical X-linked severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97042245; PubMed=8900089; Stephan V., Wahn V., Le Deist F., Di. Mueller-Fleckenstein I., Horneff G.,
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                                                                                                                                     morphology.
                                                                                                                                                                       "An
                                                                                                                                                                                                                                                     "B-cell-negative severe combined common gamma chain mutation."; Hum. Genet. 99:677-680(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT XSCID ARG MEDLINE=97042245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Clin.
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de Saint Basile G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95023932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [11]
VARIANT XSCID ASN-39
                                                                                                                                                                                     MEDLINE-98064061;
Sharfe N., Shahar
                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                               VARIANT XSCID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95164726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pepper A.E., Buckley R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95397841;
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                                                                                                                                                                                                                                         18]
            SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE II-2, II-4, I AND PROBABLY ALSO THE II-13 RECEPTORS.

SUBCELLULAR LOCATION: Type I membrane protein.

DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMMONDEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA,
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                                                                                                                     FUNCTION:
                                                                                                                                                                   interleukin-2
                                                                                                   INTERLEUKINS
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J.M., Pepper A.E., Bedard P.-M., Laframt ale germ line mosaicism as the origin of a-chain mutation causing X-linked severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutational hotspots in the interleukin-
causing human X-linked severe combined
J. Hum. Genet. 57:564-571(1995).
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Lester T., Genet S.,
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MMON SUBUNIT FOR THE
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P.A., Katz F.,
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M., Roifman C.M.;
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PubMed=7668284;
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70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94283267; PubMed=7516866; Chen X., Horseman N.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cropsac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
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                                                                                                                               QPPLSLDHFKECTV-EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ
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LQNIVKPLPPVYLTFTRESSCEIK---
                     LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                         FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQ
                                                               CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
                                                                                    CTNGSEVQSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNL
                                                                                                          SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR
                                                                                                                                                     TTYNITVMAMNEIGSNSS----
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IPR003961;
IPR003528;
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BY SIMILARITY:
N-LINKED (GLCNAC.
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3; Mismatches
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Pred. No. 3.
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CYTOPLASMIC
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01-FEB-1994 (Rel. 28, Las
15-JUN-2002 (Rel. 41, Las
Cytokine receptor common
(Interleukin-2 receptor g
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                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=B6.S;
                                                                                                                                                                                            chromosomal localization and expression Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                   Disanto J.P., Certain S., Wilson A., Macc
Fischer A., de Saint Basile G.;
"The murine interleukin-2 receptor gamma
                                                                                                                                                                                                                                               MEDLINE=95104285; pubMed=7805729; Disanto J.P., Certain S., Wilson A.,
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MEDLINE=93366191; PubMed=8359699;
Kobayashi N., Nakagawa S., Minami Y.,
                                                                                                                                                                                                                                                                                                                                                                                                     Cao X., Kozak C.A., Lucus V., Woguchi M., O'Connell E., Lee "Characterization of cDNAs encoding the murine interleukin (IL-2R) gamma chain: chromosomal mapping and tissue specific 11-2R gamma chain expression ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-CBA/CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of the mouse interleukin 2 receptor gamma demonstration of functional differences between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93277575; PubMed=8503926; Kumaki S., Kondo M., Takeshita T.,
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                                                                                                                 Dougherty G
                                                                                                                             MEDLINE=96341745; PubMed=8750189; Chiu R.K., Droll A., Cooper D.L.,
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                                                                                                                                                                                                                                                                                                                         "Cloning
                                                                                                     "Molecular mechanisms regulating
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                                                               e adhesion protein CD44.";
Neurooncol. 26:231-239(1995).
- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS
INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2,
AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                            of the cDNA
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EMBL; U21795; AAA6279.1; -
EMBL; D13565; BAA02760.1; -
EMBL; L20048; AAA39286.1; -
EMBL; S75852; AAB32904.1; -
EMBL; S75844; AAB32904.1; -
EMBL; S75847; AAB32904.1; -
EMBL; S75848; AAB32904.1; -
EMBL; S75849; AAB32904.1; -
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EMBL; S75849; AAB32904.1; -
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InterPro; IPR002996; (
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JN0775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinf
European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
  LERMPPIPP
                                                 LLRKPNTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PETKYQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
                                                                                                       VRSRYNPICGSSQQWSKWSQPVHWGSHTVEENPSLFALEAVLIPVGTMGLIITLIFVYCW
                                                                                                                                                           VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF--ILILVIFVTGL
                                                                                                                                                                                                          SESQLELRWK - - SRHIKERCLQYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
                                                                                                                                                                                                                                                              SSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVENE-TYTLKTTNETRQLCFV
                                                                                                                                                                                                                                                                                                                 SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL
                                                                                                                                                                                                                                                                                                                                                                     ADGQN1GCRFPYLEASDYKDFY1CVNGSSENKP1RSSYFTFQLQN1VKPLPPVYLTFTRE
                                                                                                                                                                                                                                                                                                                                                                                                                      PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA----TNLTLHYRYKVSDNNTFQECSHYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003961; FN_III.
IPR003531; Hemtopoptn_S_F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369
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                                                   370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         license agreement (See
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BY SIMILARITY
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOKINE RECEPTOR COMMON GAMMA CHAIN EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB2D5AB459077AC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212.5; DB 1
No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                       283
                                                                                                                                                           361
                                                                                                                                                                                                                                                              307
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RESULT 11
CYRG_CANFA
                                                                                                                                                                                                                                                         Matches
            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain)
                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                   InterPro; IPR002996;
InterPro; IPR003961;
InterPro; IPR003531;
SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henthorn P.S., Somberg Felsburg P.J.; "IL-2R gamma gene micro
                                                                                                                                                                                                                                                                                               EMBL; U04361; AAC48403.1; HSSP; P31785; 1ILM.
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      severe combined
disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
MEDLINE=95130114; PubMed=7829104;
                                              SEQUENCE
                                                                               CARBOHYD
                                                                                          CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                                       DISULFID
                                                                                                                                                  DISULFID
                                                                                                                                                             DOMAIN
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                     modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYRG_
                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKINS.
SUBURIT: THE GAMMA CHAIN IS COMMON TO TH
AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCCELLULAR LOCATION: Type I membrane pr
DISEASE: DEFECTS IN ILLERG ARE THE CAUSE
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEVERE COMBINED IMMUNODEFICIENCY.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: COMMON SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANFA
   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma gene microdeletion
              Similarity
                                                                                                                                                                                                                            PS01355; HEMATOPO_REC_S_F1; 1.
; Transmembrane; Glycoprotein; Signal.
                                             23
262
284
151
62
102
24
71
75
84
159
164
159
  Conservative
                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunodeficiency
                                                                  373
261
283
373
373
373
249
249
115
715
715
715
715
715
715
715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                          CR1A.
FN_III.
                                                                                                                                                                                                                                                                                                                                                     institutions as long as atement is not removed. U
                                              42516
            9.98;
                                                                                                                                                                                                                                                             Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.L., Fimiani V.M., Puck J.M.,
                                              MW;
  48;
                                           N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR
            Score 208; DB 1;
Pred. No. 7.4e-10;
                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                             FIBRONECTIN
                                                                                                                                                                                             CYTOKINE RECEPTOR COMMON GAMMA EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                       POTENTIAL
                                                                                                                                                 POTENTIAL
                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               demonstrates that o
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE
                                                        D (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373
                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ã
                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE
  108;
                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                               its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A CANINE X-LINKED
                     Length 373;
                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f the human
  Indels
                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-linked
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  40;
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Gaps
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  12;
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RESULT 12
IL3B_MOUSE
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL3B_MOUSE
P26954;
01-OCT-1993
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; RCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
30-MAY-2000 (Rel. 37, Last annotation update)
Interleukin-3 receptor class II beta chain precursor (Colony stimulating factor 2 receptor, beta 2 chain).
CSF2RB2 OR AI2CA OR IL3RB2 OR IL3R.
                                                                                                                                                                                  PIR;
                            Receptor;
SIGNAL
                                                                        Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2
                                                                                                                                                                     MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of an interleukin-3 receptor gene: a receptor gene family."; Science 247:324-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90117145; PubMed=2404337;
                                                        PROSITE; PS01355; HEMATOPO_
                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                              entities
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                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yahara I.,
                                                                                                                       InterPro;
                                                                                                                                       [nterPro;
                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itoh N., Yonehara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
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                                                                                                BL; M29855; AAA39295.1; ..
R; A40091; A40091
D; MGI:1339760; Csf2rb2.
terPro; IPR002996; CR1A.
terPro; IPR00282; Cytok_receptor_2.
terPro; IPR003961; FN_III.
terPro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: IN MOUSE THERE ARE TWO CI
RECEPTORS. ONE CONTAINS THIS IL-3-S
OTHER CONTAINS THE BETA CHAIN ALSO
AND GM-CSF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KENPLFASEAVLIPLGSMGLIISLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDRSWTEQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCGSAQRWSEWSHPIHW-GSNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PRRQSTQKLKLQNLVIPWAPENLTLHNLSESQLELSWS---NRHLDHCLEHVVQYRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCWLQKEEIHLYETFVVQLRDPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DTTLVTATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLS
                                                                                                                                                                                                                               an email to license@isb-sib.ch).
           Transmembrane;
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                            Glycoprotein; Signal.
POTENTIAL.
                                                        REC_S_F1;
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            INTERLEUKIN-3 RECEPTOR CLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.,
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01-NOV-1997 (Rel. 35, Last sequence up.
15-JUN-2002 (Rel. 41, Last annotation
Cytokine receptor common gamma chain p
(Interleukin-2 receptor gamma chain)
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DNA Ce
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   the
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MEDLINE=96268473; PubMed=8672241;
MOO J., Stone R.T., Solinas-Todo
YOO J., Stone R.T., Solinas-Todo
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Crania: Mammalia; Eutheria; Cetartiodactyla; Bovidae; Bovinae; Bos.
                   between
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                                                                                                                                                                                             loning
                                                     INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                              Cell Biol. 15:453-459(1996). FUNCTION: COMMON SUBUNIT FOR THE
                                                                                                                                                                                                                                                                                                                             taurus (Bovine).
    European
                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the S_w is SInstitute of Bioinformatics and the EMBL outstation -
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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No. 2.5e-08;
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HSSP;
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entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003961;
InterPro; IPR003531;
YTFRVRSRYNPLCGSAQHWSDWSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG
                LCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                        LPLPKVQ----CFVFNVEYMNCTWNSSSEPQP-----NNLTLHYGYRNFNGDDKLQECG
                                                                                                                                                                                                     IPETKYQDMDCVYYNWQYLLCSW-----KPGIGVLLDTNYNLFYWY---EGLDHALQCV
                                                        LRNLSEFQLELSWS - - - NRYLDHCLEHLVQYRSDRDRSWTEQSVDHRHSFSLPSVDAQKL
                                                                                   FTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVEN-ETYTLKTTNETRQ
                                                                                                                HYLFSEGITSGCWFGKKEIRLYETFVVQLQDPREHR--KQPKQMLKLQDLVIPWAPENLT
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P31785; 1ILM.
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and this statement
requires a license
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26.2%;
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                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                    POTENTIAL.

CYTOKINE RECEPTOR COMMON GA
EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                              Score 189.5; DB Pred. No. 2.5e-08
                                                                                                                                                                                                                                  Mismatches
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01-OCT-1993 (Rel. 27, Creatol-1995) (Rel. 33, Last 16-OCT-2001 (Rel. 40, Last Cytokine receptor common by CSF2RB OR IL5RB OR IL3RB.
Proc.
                "Molecular cloning of a second subunit of the recegranulocyte-macrophage colony-stimulating factor (reconstitution of a high-affinity GM-CSF receptor. Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91088571; Pubme
Hayashida K., Kitamura
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                   Miyajima A.;
"Molecular cloning
                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                  27, Created)
33, Last sequence update)
40, Last annotation update)
common beta chain precursor
                                                                                                                         PubMed=1702217;
                                                                                                         Τ.,
                                                                                                         Gorman
                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                 Hominidae;
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Kitamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59941; AAA18171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00041; fn3; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002996; CR1A.
InterPro; IPR000282; Cytok_r
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hemtopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 138981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:2436; CSF2RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39255; A39255.
HSSP; P19235; 1EBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BE
CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DATABASE: NAME-PROW; NOTE-CD guide CDw-131 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no reby non-profit institutions as long as its conterpositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm".
                            PRRAEKHIKSSV-----NI--QMAPPSLNVTKDGD-SYSLRWETMKMRYEHIDHTFEIQ
                                                                                    VASSVSFGLFYKPSPDAGEEECSPVLR---EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ
                                                                                                               VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN
                                                                                                                                                                       KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG
                                                                                                                                                                                                   GSPQSHWLSPGDLEFEVVYKRL-QDSWEDAAILLSNTS----QATLGPEHLMPSSTYVA
                                                                                                                                                                                                                                                          VIPCOSFVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL
                                                        GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE
                                                                                                                                           RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE
                                                                                                                                                                                                                               SM00060;
                                                                                                                                                                                                                                                                                                                                 Similarity
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1 16 POTENTIAL.
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97335

    to the EMBL/GenBank/DDBJ databases.
    AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5

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22.5%;
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
3398E37FDB8F393A CRC64;
                                                                                                                                                                                                                                                                                                                                Score 178.5; DB 1; Pred. No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC FIBRONECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE-III 1.
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01-OCT-1993
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DISULFID
CARBOHYD
                                                                                                                                        CARBOHYD
SEQUENCE
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MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Cytokine receptor common beta chain pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR003531; Hemtopoptn_S_F1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and expression of a gene encoding an like protein: identification of another member receptor gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90319131; PubMed=1695379; Gorman D.M., Itoh N., Kitamura T., Yahara I., Arai K., Miyajima A.;
                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M34397; AAA37204.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3,
AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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5 CLAIGCLYTFLISTTFGCTS---
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SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS
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MGI:1339759; C:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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896
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896
241
440
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                                                                    8.2%;
20.7%;
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                                                69;
                                         Score 173.5;
Pred. No. 1.5e
59; Mismatches
                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

SCE16EDFDC07A999 CRC64;
                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOKINE RECEPTOR COMMON
                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87:5459-5463(1990)
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                                                                                          DB
                                                185;
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-VNPPQDFEIVDPGYLGY
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                                                                   327 V-----KHLEQGKFIMSYNHIQMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
                                                                             214 VNGSSENKPIRSSYFTFOLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYE 273
                                                                                                                                                                                          49 LYLQWQPPL---SLDHFKECTYEYELKYRNIGSETWKTIITKN-----LHYKDGFDLNKG 100
                                                                                                                                                                                                           94 CVPRRCVIPY---TRESITNEDYYSFRPDSDLGIQLMVPLAQNVQPPLPKNVSISSSEDR 150
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Search completed: January 24, 2003, 19:36:39 Job time: 17 secs

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Copyright (c) 1993 - 2003 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution. being printed,

Result No.	Score	Query Match	Length DB	BB	ID	Description
ב	2104	100.0	380	18	AAW24972	Human interleukin-
2	2104	100.0	380	18	AAW35295	Human IL-13 bindin
ω	2104	100.0	380	18	AAW36613	Human Zcytor2 cyto
4	2104	100.0	380	19	AAW41520	Human HR-1 recepto
5	2104	100.0	380	19	AAW41502	Human cytokine/pep
6	2104	100.0	380	19	AAW33603	Homo sapiens HR-1
7	2104	100.0	380	21	AAY95296	IL-13 binding chai
8	2104	100.0	380	22	AAG63812	Amino acid sequenc
9	2104	100.0	380	22	AAY72136	Human interleukin
10	2104	100.0	380	22	AAB29748	Human IL-13 recept

27 27 28 30 30 30 30 30 30 30 30 30 30 30 30 30	
33 3 456.5 6935.5 3311.5 3111.5 3011.5 3025.5 2925.5 2925.5 292.5 292.5	2104 2078 1853 1853 11763 11753 11753 11952 1503 11992 11992 11994 11994 11994 11994
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283 255 1145 1157 396 420 420 421 420 421 420 421 420 421 420 421 420 421 420 421 420 421 420 336 420 421 420 421 420 420 421 420 420 420 420 420 420 420 420 420 420	380 372 317 315 315 316 316 316 316 316 316 316 316 317 317 317 317 317 317 317 317 317 317
222 222 223 223 223 113 113 113 113 113	
AAB29747 AAU69134 AAU69133 AAW56252 AAR22216 AAR22216 AAR22219 AAR25064 AAR22215 AAR21856 AAW21856 AAW21856 AAW21856 AAW09821 AAW24973 AAW18973 AAW18973 AAW18973 AAW18973 AAW18973 AAW24973	AAM4 9201 AAW36614 AAW36616 AAB13746 AAB13746 AAW56260 AAW56260 AAU69135 AAU69137 AAU69137 AAU69138 AAU69141 AAU69141 AAU69140
2000555555	Human IL-13R alpha Human Zcytor2 Cyto Celebus macaque Zc Glebus macaque Zc Human soluble cyto Mature interleukin Construct containi Canine interleukin Canine interleukin Canine IL-13R extr Canine IL-13Ralpha Canine IL-13Ra

# ALIGNMENTS

X P P T X	DR DR	X P I	PA	XX XX	Y PF	X PD	XX	XX SO S	X X X	XX	XX X	XX OA	RESU AAW2 ID XX
New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc	WPI; 1997-319773/29. N-PSDB; AAT85826, AAT86464.	Caput D, Ferrara P, Laurent P, Vita N;	(SNFI ) SANOFI SA.	06-DEC-1995; 95FR-0014424.	07-NOV-1996; 96WO-FR01756.	12-JUN-1997.	WO9720926-A1.	Homo sapiens.	<pre>Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.</pre>	Human interleukin-13 beta receptor.	22-JUN-1998 (first entry)	AAW24972;	RESULT 1 AAW24972 AAW24972 standard; protein; 380 AA. XX

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AAW3529
ID AAW3
XX AAW3
XC AAW3
XX DT 27-M
DT 27-M
DE Huma
XX Inte
KW medi
XX inte
KW alle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             affinity, but acquires high affinity when associated with the IL-4 receptor. Nucleic acids encoding II-137 beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant II-138 beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and
                     allergy; asthma;
                                      Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
                                                                                                                                    27-MAR-1998
                                                                                                                                                                                                            AAW35295 standard; Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and 427 aa proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to new purified peptides comprising 380 or 427 amino acid sequences, which are receptors for interleukin-13 (IL-13); the 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence
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                                                                                           Human IL-13 binding chain of the IL-13 receptor.
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                                                                                                                                                                                                                                                                                                                           LLLRKPNTYPKMIPEFFCDT 380
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                                                                                                                                                                                                                                                                                                        LLLRKPNTYPKMIPEFFCDT 380
                                                                                                                                                                                                                                                                                                                                                                                TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVYLTETRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLVTATVENETYTLKTTNE
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                                                                                                                                  (first entry)
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                     immune complex disorder.
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Pred. No. 2e-197;
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                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding interleukin-13 receptor binding chain and transformed cells - proteins, antibodies and inhibitors, for treating immunoglobulin E-mediated diseases, e.g. Graves disease and in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Peptide
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                                                        SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
                                                                                                             ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                      SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
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342..362
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1..25
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/note= "putative"
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This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and was isolated from human placental polyA+ RNA. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of II-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of
                                                                                                                                                  Claim 2;
                                                                                                                                                                      New nucleic acid encoding testis-specific cytokine receptor - use for identification of ligands or antagonists, potentially for use male contraceptives or for infertility treatment
                                                                                                                                                                                                                     WPI; 1997-470820/43.
N-PSDB; AAT96782.
                                                                                                                                                                                                                                                     Baumgartner
O'Hara PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine receptor; ligand binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Zcytor2
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                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                Page 47-48; 79pp; English.
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364..380
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                                                               (SMIK ) SMITHKLINE BEECHAM CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mat_protein
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Pred. No. 2e-197;
Mismatches 0
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Best Local S
Matches 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 52% similarity to the interleukin-5 receptor. Its amino acid consequence was deduced from a cDNA clone (see AAV04131) obtained from a chuman testis library. Recombinant HR-1 receptor can be expressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoietic disorders, e.g. where induced by AIDS, aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor overexpression. The antibodies can also be used to determine HR-1 receptor levels, since overexpression may be diagnostic of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequence encoding human cytokine peptide hormone receptor - useful to treat, prevent or diagnose, e.g. lowered resistance to infection, asthma, allergy or haematopoietic disease
HR-1 receptor; cytokine receptor;
infection; burn; trauma; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                        08-JUN-1998
                                                                                                                               AAW41502 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and 52% similarity
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                                         Human cytokine/peptide receptor, HR-1 receptor.
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DB; AAV04131.
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                                                                                                                                                                                                                                LLLRKPNTYPKMIPEFFCDT
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                                                                                                                                                                                                                                                                                                                  PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
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380; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Page 62-64; 76pp; English
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                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a novel human cytokine/peptide hormone he HR-1 receptor, that shows 27% identity
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; peptide hormone recepto
allergy; AIDS; aplastic
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. 2e-197;
0;
              receptor; human;
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receptor, designated HR-1 receptor. The amino acid sequence was deduced from a cDNA clone (see AAVOA075) isolated from a human test is cDNA library. It shows 27% amino acid identity and 52% similarity with the human interleukin-5 receptor. Also claimed are polynucleotides encoding HR-1 receptor, vector and host cells, an agonist to the polypeptide, antibody against the polypeptide, an atlagonist that inhibits the activity of the polypeptide, an antagonist that inhibits the activity of the polypeptide, a process for diagnosing a disease, or a susceptibility to disease, related to expression of HR-1 receptor, and a method for identifying compounds that activate or inhibit the HR-1 receptor. HR-1 receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of cyclic neutropaenia or as a consequence of cytotoxic therapy of cancer, lymphoma, leukaemia and/or bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                               Best Local
Matches 3
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(SMIK ) SMITHKLINE BEECHAM CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This protein comprises a novel human cytokine/peptide hormone
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                                                                        HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
                                                                                                                                                                                                                                                                            MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
                          ALQCVDYIKADGQNIGCREPYLEASDYKDEYICVNGSSENKPIRSSYETEQLQNIVKPLP
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Pred. No. 2e-197;
Mismatches (
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Peptide
                                                                                                                                                            DNA encoding human cytokine-peptide hormone receptor - use treating preventing or diagnosing, e.g. lowered resistance infection, asthma, allergy, or haematopoietic disease
                  receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. those listed above. Antibodies may also be used to assay levels of HR-1 receptor, overexpression of which may be diagnostic of tumours, by usual immunoassays; to isolate and identify HR-1 receptor-expressing cells; or for affinity purification of the HR-1 receptor.
                                                                         The sequence is that of the human cytokine/peptide hormone receptor (HR-1 receptor). This, or it's activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoietic disorders, e.g. where induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. Antagonists of the
                                                                                                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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 Sequence
                                                                                                                                             Claim 15; Fig 1; 75pp; English
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12-JUN-1996;
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DB; AAV02295.
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SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                            allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                           hormone receptor; AIDS; acquired immune deficience aplastic anaemia; neutropaenia; cancer treatment; resistance; diagnosis; tumours; HR-1 receptor; llergic; haematopoietic; disorder
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96US-0017843
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Best Local Similarity
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13-DEC-1999;
                  22-JUN-2000
                                     WO200036103-A1
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99WO-US29493.
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MAFVCLAIGCLYTELISTTEGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
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                                                                             PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYBIBIREDDTTLVTATVENETYTLKTTNE
TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                              PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
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Pred. No. 2e-197;
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cytokine receptor; haematopoietin receptor; atopy; allergy; asthma; immune complex disease; lupus; nephritis; thyroiditis; Grave's disease; inflammatory; infection; therapy; antiallergic; antiinflammatory; antiasthmatic; vaccine. Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse; chain of human IL-13 receptor.

"extracellular domain; a polypeptide "intracellular domain; a polypeptide comprising amino acids 257-383 is specifically claimed in Claim 11(f) specifically claimed comprising amino acids 22-334 domain" 'n Claim 1S 11(e)" 11(f)"

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis, thyroiditis and Grave's disease), lung inflammation, immunodeficiency, and cancer. Since II-13 inhibits macrophage activation, II-13bc proteins can also be used to enhance macrophage activation, e.g. in vaccination, treatment of mycobacterial or intracellular organisms or parasite infections. II-13bc proteins may also be used to potentiate the effects of II-13 in vitro and in vivo, as diagnostic agents, and to screen for agents capable of binding to II-13bc or II-13 receptor, or which interfere with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11(d); Page 53-54; 60pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding an interleukin-13 (IL-13) binding chain an IL-13 receptor for treating IgE-mediated conditions, such as atogasthma, Grave's disease and inflammatory conditions of the lung -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding
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DB; AAA27912.
                                                                             TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
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                                                               TROLCEVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLREWLPFGFILILVIFVTG
                                                                                                                                         PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
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Pred. No. 2e-197;
Pred. No. 2e-197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stimulating immune response against interleukin-13 receptor alpha2 subunit in a subject having or at risk of developing gliomas, invoformulating a vaccine comprising an agent that stimulates immune
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       risk of developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha 2 (IL-13Ralpha2), which is a cancer/testis antigen. The specification describes a method for stimulating immune response against IL-13Ralpha2 subunit. The method is used for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human interleukin-13 receptor subunit
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                                                                                                                                                                                                                                                                                                                                                                                                        treating
                                                                                                                                                                                                                                                                                                                                                                                                                     immune response against IL-13Ralpha2 in a human being having or at risk of developing a cancer having glioma cells expressing IL-13Ralpha2. The polypeptides and polynucleotides are useful for preventing and/or
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                              PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                           ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                                                                                                                       SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
                                                                                                                                                                                                      HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
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DB; AAH74791.
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                                                             ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-13 receptor subunit alpha 2;
antigen; immune response; glioma cell.
                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 2e-197;
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RESULT 9
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Wills-Karp
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                                                                         Claim la; Page 69-70; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
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    invention relates to a method of treating, or inhibiting formation of tissue fibrosis in mammals, which involves
                                                                                                                                                                                                                      2001-080753/09.
DB; AAD02335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLRKPNTYPKMIPEFFCDT
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                                                                                                                                                                                                                                                                                                                                                             GENETICS INST INC. UNIV JOHNS HOPKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of an expressed sequence tag (EST) identified
as yg99f10.rl human cDNA clone 41648 5"
26..380
/label= Mature_human_interleukin (IL)-13_binding_chain_
of_IL-13_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "This region is identical to the translated sequence of an expressed sequence tag (EST) identical as yg99f10.rl human cDNA clone 41648 5"
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    02-NOV-2000
                                                                                                                                                                                                               Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; v
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB29748
                                                                                                                                                                  wound healing; schistosoma cartilage; cardiac tissue;
                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                    AAB29748;
                                                   WO200064944-A1
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                                                                                                                                              intestinal tissue;
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                                                                                                                                                                                                                                                                                      IL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 380
                                                                                                                                                                                                                                                                                 receptor IL-13 binding chain (IL-13bc).
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vascular tissue;

infection; liver; skin; muscle; lung tissue; uterine tissue;

neural tissue.

fibrosis inhibition;

vulnerary;

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administering a pharmaceutical composition comprising interleukin (IL)-13 antagonist. The protein of the invention is useful for treating tissue fibrosis resulting from infection with Schistosoma or from healing of a wound which is a surgical incision, or inhibiting formation of tissue fibrosis which affects tissues such as liver, skin epidermis and endodermis, muscle, tendon, cartilage, cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of various II-13 related conditions such as allergic conditions, nephrotic syndrome, thyroiditis, Grave's disease and cancer. The present sequence is human interleukin (II)-13 binding chain of II-13 receptor (II-13b). II-13bc protein is used to potentiate the effects of II-13. This protein is also used to enhance macrophage activation and hence can be used in vaccination or treatment of mycobacterial or parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       testis, ovary, adrenal gland, artery, vein, colon, small ir billary tract and gut. It is also used in the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 380; Conser
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                               LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                                                                                                                                                                                               HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                                 TROLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                       PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                                                             TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                    PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
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Pred. No. 2e-197;
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Best Local S
Matches 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of treating fibrosis in a mammal by administering an interleukin-13 (IL-13) antagonist or an IL-4 antagonist. In particular, the IL-13 antagonist is the IL-13 binding chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or soluble fragments thereof. The method is useful for treating or inhibiting the formation of tissue fibrosis resulting from the healing of a wound, including a surgical incision wound, or from infection with schiscosoma. The method may be used to treat fibrosis in a variety of tissues, particularly liver tissue, but also skin epidermis, skin
                                 AAM49201 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic tissue, lung tissue, uterine tissue, neural tissue, testis, ovary, adrenal gland, artery, vein, colon, small intestine, biliary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or inhibiting tissue fibrosis resulting from infection with schistosoma and wound healing involves administering interleukin-13 or interleukin-4 antagonist -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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tissue. The present sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 76-77; 82pp; English.
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                                                                                                         LLLRKPNTYPKMIPEFFCDT
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DB; AAC81416.
                                                                                                                                                                                       TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                  PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
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                                                                                                                                                                     TRQLCEVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLREWLPEGFILILVIFVTG
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MJ, Wood C;
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                                Protein; 380
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matches 0;
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The invention relates to the use of a nucleic acid or vector CC encoding a polypeptide with at least 70% identity to interleukin-13 CC receptor alpha-2 chain (IL-13R alpha-2; AAM49201) for rendering a CC cancer cell sensitive to IL-3R-targeted immunoconjugates or for CC inhibiting the growth of a cancer cell. In some cancers that exhibit CC little or no expression of IL-13R transfection with the IL-13R CC alpha-2 chain is sufficient to inhibit growth, while in CC other such cancers, the introduction of the IL-13R alpha-2 chain enables immunoconjugates (such as immunotoxins) that comprise IL-13 to be CC in the inhibition or death of cells in the invention also results CC in the inhibition or death of cells in the tumour which were not CC in the inhibition of at least some of the cells of a tumour with the IL-13R alpha-2 chain causes the secretion of a cytokine or other factor that CC alpha-2 chain causes the secretion of a cytokine or other factor that CC alpha-2 chain activated to kill the tumour cells. Because a nucleic acid encoding just the IL-13R alpha-2 chains of the entire IL-13R, the CC choice of vectors that can be used for transfection. A wide range of CC cancers can be treated using the methods of the invention, including CC brain cancer, head and neck cancer (preferably sequenous cell carcinoma), breast cancer, postate cancer, testicular cancer, skin cancer, cervical blader cancer, crevical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of nucleic acid or vector encoding interleukin-13 receptor alpha chain polypeptide that binds IL-13, for sensitizing a cancer cell e.g brain cancer cell to effector molecule or inhibiting growth of cancer
                                                                                                                   bladder cancer, prostate cancer, testicular cancer, skin cancer, cancer, uterine cancer, or sarcoma. The present sequence represent the human IL-13R alpha-2 chain which is specifically claimed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mesothelioma; pancreatic; colon; gastric; ovarian; renal; bladder;
prostate; testicular; skin; cervical; uterine; sarcoma; cytostatic;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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DB; ABL55245.
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                                                                              The present sequence is not shown in the specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page -; 80pp; English
                                                                                                nan IL-13R alpha-2 chain which is the method of the invention.
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  380
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                                                                                                                                     present sequence represents
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Query Match Best Local Si Matches 380;

Similarity

100.0%; 100.0%; tive 0;

Score 2104; DB 23; Pred. No. 2e-197;

Length

380;

Mismatches

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Gaps

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Conservative

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ID AAW36
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shares homology with cytokine receptors and was isolated from a human testis cDNA library. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or
                                                                                                                                                                           male
                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                       Baumgartner
O'Hara PJ;
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                                                                                                                                                                     nucleic acid encoding testis-specific cytokine receptor - identification of ligands or antagonists, potentially for e contraceptives or for infertility treatment
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MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
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                                                                                                Key
Protein
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18-SEP-1997
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377; Conservative
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RESULT 14
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                                                                                                                                     AAE13746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding testis-specific cytokine receptor -
for identification of ligands or antagonists, potentially for
male contraceptives or for infertility treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baumgartner O'Hara PJ;
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Pred. No. 7.4e-173;
7; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to an isolated soluble zalphall cytokine receptor CC polypeptide and their cDNA molecules. Zalpha proteins are useful for CC inhibiting or antagonising the ligand activity-induced proliferation of CC haematopoletic cells and haematopoletic cell progenitors preferably CC lymphoid cells which are natural killer cells or cytotoxic T cells. CC Zalpha is useful for treating immune and inflammatory disorders, for CC reducing proliferation of neoplastic B or T cells, for suppressing an CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is CC useful for treating diseases that require immune regulation including CC useful for treating diseases that require immune regulation including CC useful for treating diseases that require immune regulation including CC useful gravis, systemic lupus erythematosus (SLE) and diabetes; CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; CC asphis, viral infection (dengue virus infection) and cancer. The present CC sepsis, viral infection (dengue virus infection) and cancer. The present CC sepsis, viral infection (dengue virus infection) and cancer. The present CC sepsis, viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer. The present CC sepsis viral infection (dengue virus infection) and cancer wirus infection (dengue virus infection) and cancer wirus infec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel soluble receptor polypeptides and polynucleotides used cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immuresponse in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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28-JUL-2000;
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                                             YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIP
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                                                                                                            YYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD
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                                                                                                                                                                                                        KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV
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2000US-222121P.
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Pred. No. 3.1e-164;
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Best Local Similarity
Matches 315; Conserv
                                                                                                                                                                                                                       The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-207062/18.
N-PSDB; AAV22702.
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10-SEP-1996;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                         Disclosure; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                  New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection {\sf Conditions}
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilton DJ, Nicola NA,
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isease; antibody; immunotherapy.
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sp_bacteria:*
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sp_unclassified:*
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Q14631
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Q88786 mus musculu
Q8vhk6 rattus norv
Q90xp8 oncorhynchu
Q14631 homo sapien
Q14631 homo sapien
Q14631 fomo sapien
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131	135	138	143.5	145.5	146.5	147.5	151	151	151	151	151	153	153.5	155	156	159	164	167	170	173.5	174.5	175.5	178	185.5	187	187	212.5	222
6.2	6.4	6.6	6.8	6.9	7.0	7.0	7.2	7.2	7.2	7.2	7.2	7.3	7.3	7.4	7.4	7.6	7.8	7.9			æ .ω	8.3	8.5	8.8			10.1	10.6
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Q9BEG2	093404	Q9UEH7	Q9JM58	075462	Q9UHH5	Q9DFU0	Q96P35	д9инл5	Q96P36	Q8TD78	Q16354	046386	Q9W6U9	Q90WG7	Q9xS92	Q99JZ1	Q9GLW3	Q9N0J7	Q9Z1A0	057519	Q9PTH9	Q8QZX9	Q64146	Q9DEQ1	Q9PTI0	Q9IBF6	Q8VHR8	Q8SQ71
Q9beg2 bos taurus	093404 oreochromis	homo	Q9jm58 mus musculu	075462 homo sapien	Q9uhh5 homo sapien	0 spa	homo	homo	homo		Q16354 homo sapien	=	Q9w6u9 gallus gall		Q9xs92 trichosurus	Q99jzl mus musculu		C	cavia po	xenopus			Q64146 rattus norv	oncorhy	xenopus		Q8vhr8 rattus norv	Q8sq71 sus scrofa

### ALIGNMENTS

δã Вþ Qy 밁 Q95LF0 RESULT 1 Matches 272; Query Match Best Local S Q95LF0; 01-DEC-2001 01-DEC-2001 01-MAR-2002 Vet. Immunol. Immunopathol. 79:181-195(2001).
EMBL; AF31453; AAL14887.1; -.
InterPro; IPR002996; CRIA.
InterPro; IPR002996; CRIA.
PROSITE; PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1. Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
MCBI\_TaxID=9615; Q95LF0 "Molecular cloning of canine IL-13 receptor alpha chain (alphal and alpha2) cDNAs and detection of corresponding mRNAs in canine MEDLINE=21287533; PubMed=11389954; Canis familiaris (Dog). 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin 13 receptor alpha chain 2. tissues."; SEQUENCE Receptor 60 NFKECTIEYELKYRNIDSENWKTIITKNLHYKDGFDLNKGIEAKINTLLPAQCTNGSEVR 61 HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120 MAFIHLDVGFLYTLLVCTAFG-SMLSNAEIKVNPPQDFEIVDPGYLGYLSLQWQPPLFPD Similarity 386 AA; Conservative PRELIMINARY; 71.4%; Score 1503; DB 6; 72.9%; Pred. No. 1.2e-121; rative 42; Mismatches 57; 45110 MW; A16FDF2DD023ED95 CRC64; Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis. 386 ð Length 386; Indels 2; Gaps 59 ?

8 10 11 12 12 13 14 15

Q96BB4 1 Q8VHC2 Q15469 1 Q920B8 097597

Q9z0k4 cavia porce
Q9s0b4 homo sapien
Q8bbc rattus norv
Q15469 homo sapien
Q920b8 rattus norv
Q97597 bos taurus
Q9ps3 rattus norv
Q9udy5 homo sapien
Q8wx09 homo sapien

Q9Z0K4

Q9UDY5

Q99PS3

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                                                                                                                                                                                                     Query Match
Best Local S
Matches 219
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STRAIN-C3H/HEJ; TISSUE-THYMUS;
MEDLINE-98391042: PubMed-9725226:
Donaldson D.D., Whitters M.J., Fitz L., Neben T.]
Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turr
Collins M.;
"The murine IL-13 receptor alpha 2: molecular clc
characterization, and comparison with murine IL-
J. Immunol. 161:2317-2324(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            088786;
01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2001) to the ENEL; U65747; AAC33240.1; -. EMBL; BC003723; AAH03723.1; -.
                                                                                                                                                                                                                                                                                                            InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
Submitted (
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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MGD; MGI:1277954; Ill3ra2.
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219; Conserv
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tor alpha 2 (
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Rodentia;
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                                                                                                                                                                                                                                                                             44482 MW;
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Last sequence up
Last annotation
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                                                                                                                                                                                                     Score 1194.5;
Pred. No. 5.3e
55; Mismatches
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Sciurognathi; Muridae;
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Turner
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Best Local S
Matches 211
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Q8VHK6;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of rat interexpression in rat tissues.";
submitted (NOV-2001) to the EME
EMBL; AF448818; AAL57513.1; -.
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InterPro; IPR003532; Hemtopoptn_S_F2
PROSITE; PS01356; HEMATOPO_REC_S_F2;
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                        TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
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                                                                                                                                                                                                                                 ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
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11; Conservative
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
13 receptor alpha chain 2.
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Q14633;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. MCBI_TaxID=8022;
  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Interleukin-5 receptor precursor.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Interleukin 13 receptor alpha-2.
                                                                           Homo sapiens
                                                                                                  HSIL5R.
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                           3 (Human).
Chordata;
Chordata;
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Pred. No. 7.6e
74; Mismatches
                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               PRT;
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.6e-42;
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RESULT
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01-NOV-1996
01-MAR-2002
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SEQUENCE
                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                   Q14631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; PubMed-1732409;
Murata Y., Takaki S., Migita M.,
                                       TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; PubMed=1732409;
MUTATA Y., Takaki S., Migita M., I
"Molecular cloning and expression
                                                                                                                                                                                                         Q14631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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InterPro; IPR003532; Hemtopoptn_S_F2.
PROSTTE; PS01356; HEMATOPO_REC_S_F2;
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           EMBL;
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                               receptor
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                             01-MAR-2002 (TrEMBLrel.
Interleukin-5 receptor
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Local Similarity
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          Exp. Med. : BL; X61177;
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                                                                                                                                                                                                                                                                                            LRKPNTYPKMIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
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                                                                                                                                                                                                                                                                                                                 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
                                                                                                                                                                                                                                                                                                                                                           EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                                                                                                                                                                                                                                                                                                ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV
                                                                                                                                                                                                                                                                                                                                                                                                      LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                                                                                                                                                                                                                                                                                           -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNIVKPLPPVYLTFTR
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175:341-351(1992).; CAA43484.1; -. R002996; CR1A.
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Last annotation update
2 precursor.
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Pred. No. 9.9e-19;
9; Mismatches 156;
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; 8DC56DFC8BEFF524 CRC64;
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                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
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                                        Y., Tominaga A., human interleukin
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                                                                                                                     Homo
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RESULT 7
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Canis familiaris (Dog).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Car
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SIGNAL
                                                                                           Receptor.
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01-MAR-2002 (TrEMBLrel.
Interleukin 13 receptor
                                                                   SEQUENCE
                                                                                                                                                               InterPro; IPR003532; Hemtopoptn_S_F2
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                           Vet. Immunol. Immunopathol. 79:181-195(2001).
EMBL; AF314532; AAL14886.1; -.
Interpro; IPR002996; CRIA.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=21287533; PubMed=11389954;
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PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                       PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                      tissues."
                                                                                                                                                                                                                                                                                                                              alpha2) cDNAs and
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396
44998
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                                                                   46328 MW;
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19, Last sequence update)
20, Last annotation update)
alpha chain 1 (Fragment).
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Pred. No. 1.1e
70; Mismatches
Score
Pred.
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INTERLEUKIN-5 RECEPTOR
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                                                                   926E1AC7BE5E3F42 CRC64;
                                                                                                                                                                                                                                                                                                                         C-13 receptor alpha chain (alphal corresponding mRNAs in canine
302.5; DB 6;
No. 5.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405
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hes 156;
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Q9Z0K4;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1996) to the EMBL/GenBank/DDBJ c
EMBL; U55215; AAD09361.1;
InterPro; IPR002996; CRIA.
InterPro; IPR003932; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and Characterization of the Guinea Pig Interleukin-5 alpha \mathtt{cDNa.}^{\,\mathrm{m}}_{\,\,\mathrm{c}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPIL-5RA.
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                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norris T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10141;
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                                                                       NLNYHVKINTPQEEDYE---TRNTQSKCETTLHQGVSASVRTIL-WH--GHSLLASSWVS
                                                                                                                                                                                                                       LAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKEC
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                       TTYWISPOGIPETKVQDMDCV----YYNWQ----YLLCSWKPGIGVLLDTNYNLFY-
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(TrembLrel. 10, Last seq
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Last annotation update)
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                                                                                                                                                                                                                                                                                            Score 298.5; DB Pred. No. 1.3e-17
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
INTERLEUKIN-5 RECEPTOR ALPHA
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Hystricognathi; Caviidae; Cavia.
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Interleukin 13 receptor, alpha 1 (BB12804.2.1).
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; BC015768; AAH15768.1; - EMBL; AL391280; CAD21446.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96BB4
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003393; Hemtopoptn_S_F2
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawlor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 31-427 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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IVKPLPP--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTA
                                                                                                                                                                                                    CPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--S
                                                                                                                                                                                                                              CLAIGC-LYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEI-REDDTTLYTA
                                       SLEKIHQC-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTS
                                                                GLDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQN
                                                                                           EKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHR
                                                                                                          EVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYE
                                                                                                                                              NCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLTAVLCFILLIFFFLCRIYHLWTKMFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLFDTQAIDQPNPPMDVTAETEGS-RLSIQWQKPVSAFPIHCFEYEVKICNTKDYYQVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGPWTE-----ECQEYSKDTLSRNTACWFPRTFIHSKARDRLAVHVNGSSNHATIKPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEH-KAPPGSPGTSIVNLTCTTNTAASNYTNLKSYEVSLHCTWLAGKDAPEDTQYFLYYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -WYEGLDHALQCVDYIKAD-GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSY
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OCT-2001)
                                                                                                                                                                                                                                                                                                              427
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                        ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                              48676 MW;
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                                                                                                                                                                                                                                                      14.1%; Score 297; DB 4; Length 427; 26.3%; Pred. No. 1.8e-17; Live 63; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                             E6A42F7466A39A09 CRC64;
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Best Local S
Matches 97
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STRAIL-FISHER F344;
MEDLINE-21458304; PubMed=11573960;
MEDLINE-21458304; PubMed=11573960;
Pierrot C., Beniguel L., Begue A., Khalife J.;
"Expression of a functional IL-13Ralphal by rat B cells.";
Biochem. Biophys. Res. Commun. 287:969-976(2001).
EMBL; AY044251; AAK94870.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VHC2
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002996; CRIA.
InterPro; IPR003532; Hemtopoptn_S_F2.
PR0SITE; PS01356; HEMATOPO_REC_S_F2;
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                                                                                                                                                                                                     LQCTWHNLSYMKCSWLPGKNTSPDTNYTLYYWYSSLGKSLQC-ENIHREGQHIGCSFKLT
                                                                                                                                                                                                                  MDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYL
LIIPVFVAVVII
                       LILVIFVTGLLL
                                                  VYTVRVRVKTNKLCF - - -
                                                                         TYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFI
                                                                                                                     PLGPIPARCFDYEIEIREDDTT------
                                                                                                                                                   KVESNYEHHNIQIMVKDNAGKIRPSYKIVSFTSNVKPGPPHIKHLFLKNGA--LFVQWKN
                                                                                                                                                                   TKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWAETTYWISP--QGIPETKVQD
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                                                                                                                                                                                                                                                                                                         EVQPPVTNLSVSVENLCTIVWTWSPPEGAS--PNCSLRYFSHFDDQQDKKIAPETRR---
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                                                                                                  PQN-FSSRCLSYEVEVNSTQTDSYNSNSLEVEEDKCQNSEFDRNMEGASCFISPGVLANT
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21,
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Last annotation update)
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Pred. No. 2.2e-17;
                                                 -DDNDLWSNWS-----EALSIGKEPNSTFYTT--ML
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RESULT 11 Q15469 ID Q1546

Q15469

PRELIMINARY;

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01:NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
Soluble interleukin-5 re
                                                                                              Q920B8 PRELIMINARY; PRT; 414 AAA.
Q920B8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin-5 receptor alpha.
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TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; PubMed-1732409;
Murata Y., Takaki S., Migita M., Kikuchi
"Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL CHAIN
 Pierrot C., Begue ,
"Molecular cloning
                        STRAIN-F344;
                                    SEQUENCE FROM N.A.
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003532; Hemtopoptn_S_F2.
PROSTTE; PS01356; HEMATOPO_REC_S_F2;
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EMBL; X62156; CAA44081.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Homo sapiens (Human).
                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                    EIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETROLCFVVRSKV
                                                                                                                                                                                                                                                                                                                             IACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPEDQLFALHAIDQINPPLNVTAEIEGT-
                                                                                                                                                                                                                                                                                                                                                                           TNTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
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333 AA;
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333
37722
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                                                                        Rodentia;
                                                                                   Chordata;
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28.0%;
 Szpirer C., Capron characterization
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01, Last sequence update)
20, Last annotation updat
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                                                                     Craniata; Veri
Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8D9239845E16985B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-5 RECEPTOR
 of rat IL-5Ra
                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                        Muridae;
                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tominaga A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                       Murinae;
gene
             Khalife
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takatsu
n 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                        Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                              312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SO SO
Query Match
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Best Local :
                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        097597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel 10, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
Interleukin-13 receptor alpha-1 chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2000) to the EMBL/GenE
EMBL; AF324L53; AAK97344.1; -.
InterPro; IPR002996; CR1A:
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2;
                                                                                                                                                                                                                            bovine cells.";
Vet. Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=20080132; Pubmed=10614495;
                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                   PROSITE;
                                                                                                                                                                                                         EMBL; AF074402;
                                                                                                                                                                                                                                                                        Trigona W.L., Brown W.C., Est
"Functional implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosomal mapping, analysis of the 5'-upstream
by B cells.";
                                                                                                              Receptor.
                                                                                                                                                            InterPro;
                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEWHLIVLPTAICFILLIF -- SLICRVYHLWTRLFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDQVNPPMNVTVEIENN-SLYIQWGKPLSAFPVHCFKYKLKIYNTKNGYSQMENLVTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT-----TLVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQP-----PLSLDHFKECTVEYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REW----LPEGFILILVIEVTGLLLRKPNTYPKMIP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISKIDDVSTYSIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLDHALQCVDYIK-ADGQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPGSSGTSVMNLTCTTNTVKSSHTHFRPYQVSLRCTWLVGKDAPEDTQYFLYYRFSVWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQGIPETKVQDMDCV-----YYNWQY-LLCSWKPGIGVLLDTNYNLFY----WYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SATLHADLLSPEKELLLPPVNFTIKATG-LAQVPLHWDPNPDQDPVDLKYHVKINVPQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ECQEYSRDALNRNIACWFPRTFINSKGFEQLAVHINGSSKHAAIKPLDQLFTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                     PS01356;
                                                                                                                         IPR002996; CR1A.
IPR003532; Hemtopoptn_S_F2.
PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                          349
349 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA; 47075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TKNTESKCVTPLHEGFAASVRTILK---SIHSPLASSWVSAEL-KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                            ΑĄ,
                                                                                                                                                                                                      AAC98147.1;
                                                                                                                                                                                                                                                                                                                                                                                                             Bos.
                                                                 1
349
                                                                                                                                                                                                                                                                                             W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                          39644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%;
12.6%;
                                                                                                                                                                                                                                                                                             Estes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VRAAVSSPCRMSGSWGEWS-QPIYVGK---KKKPL
                                                                                                                                                                                                                            72:73-79(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 268;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                        signaling
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4340F42F47297D84
                                            D61A4C918B1940A6 CRC64;
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                                                                                                                                                                                                                                                                                             D.M.;
264.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN_1
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.5e-15;
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DB
                                                                                                                                                                                                                                                                          the
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Length
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349;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovoidea;
                                                                                                                                                                                                                                                                        complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
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1

Best Local Matches

Similarity 24.4 83; Conservative

24.4%;

135;

Indels

59;

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RESULT COPERS CO
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DR
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FT
FT
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099PS3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin-5 receptor alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AB056101; BAB32866.1; •.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003532; Hemtopoptn_S_F2.
SMART; SM00060; FN3; 2.
PROSITE; PS01336; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99PS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishihara K., Asai K., Ohuchi K.;
"Identification of cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ
                                     PQGIPETKVQDMDCV------YYNWQY-LLCSWKPGIGVLLDTNYNLFY-----WYE
                                                                                                                                                                                                 SATLHADLLSPEKFLLLPPVNFTIKATG-LAQVLLHWDPNPDQDPVDLEXHVKINVPQED
                                                                                                                                                                                                                                 STTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQP-----PLSLDHFKECTVEYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPLTSHVKP-DPSHIKNLSFQNGDLYVQWTNPQN-FQSQCLCYEVEVINSHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLYTATVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYWHNSLGKILQCENFYR-EGQHIACSFNLTKVKDSSFEQHSVQVMVRDNAGKISPSFNI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD - - YKDFYICVNGSSENKPIRSSYFT
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PPGSSGTSVMNLTCTTNTVKSSHTHFRPYQVSLRCTWLVGKDAPEDTQYFLYYRFSVWTE
                                                                                                                                                  KYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NETYTLKTTNETR------QLCFVV------RSKVNIYC-SDDGIWS
                                                                                                                                                                                                                                                                                                         101;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                           18
414 AA;
                                                                                                                                                                                                                                                                                                    12.3%; Score 259; DB 11; larity 25.5%; Pred. No. 3.3e-14; Conservative 65; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QAMSIGQKANQTEYIT--TLLIIPVIVAAAVI
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                                                                                               -TKNTESKCVTPLHECFAASVRTILK---SIHSPLASSWVSAEL-KA
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                                                                                                                                                                                                                                                                                                                                                                                                         47108 MW;
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POTENTIAL.
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Sciurognathi; Muridae;
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RESULT 15
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Wada M., Hisano T., Kuwano M.; Submitted (JUN-1999) to the EM EMBL; U81380; AAD00511.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin-13 receptor soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002996; CRIA.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01336; HEMATOPO_REC_S_F2; UNKNOWN_1.
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                                                                                                                                                                                                                          LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEWHLIVLPTAICFILLIF -- SLICRVYHLWTRLFP
                                                                          CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDQVNPPMNVTVEIENN-SLYIQWGKPLSAFPVHCFKYKLKIYNTKNGYSQMENLVTNK
HIKNLSFHND----DLYVQWENPQNFI-SRCLFYEVEVNNSQT
                                                       C-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
                                                                                                             EKC -- ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ
                                                                                                                             ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
                                                                                                                                                                  SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV 114
                           --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT
                                                                                                                                                                                                                                                                                 Similarity 78; Conserv
                                                                                                                                                                                     -ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ECQEYSRDALNRNIACWFPRTFINSKGFEQLAVHINGSSKHAATKPLDQLFTLY
                                                                                                                                                                                                                                                                                                                                        279 AA;
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPFGFILILVIFVTGLLLRKPNTYPKMIP
                                                                                                                                                                                                                                                                                                                                        31658 MW;
                                                                                                                                                                                                                                                                                 11.5%; Score 241.5; DB 4; 27.7%; Pred. No. 6.7e-13; tive 45; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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1 MAFVCLAIGCLYTFL
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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***************************************	loubomia inhihitor	interleukin-3 rece	ᠿ	prolactin receptor	glycoprotein 130 -		prolactin receptor					=	ĸ	prolactin receptor			cytokine receptor	interleukin-3 rece	еþ	w	interleukin-2 rece	interleukin-2 rece	င္ပ		interleukin-5 rece	Се	5	1 pro	interleukin-5 rece	ייייייייייייייייייייייייייייייייייייייי	Description	

R;Murata, Y.

R;Murata, Y.

A;Reference number: S78107

A;Reference number: S78107

A;Accession: S78107

A;Accession: S78107

A;Molecule type: mRNA

C;Kesidues: 1-128,'I,130-332,'K' <MU4>

A;Coross references: EMBL:X62156; NID:936465; PIDN:CAA44081.1; PID:936466

C;Keywords: alternative splicing; cytokine receptor; 9lycoprotein; transmembrane prot

F;1-20/Domain: signal sequence #status predicted <MAT>

F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

A;Reference number: S78106 A;Accession: S78106 A;Molecule type: DNA A;Residues: 1-128,'I',130-395,'I' <MUW> A;Cross\_references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

submitted to the EMBL Data Library, July 1991 A; Reference number: S78106

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
107.5	107.5	109.5	109.5	110	111.5	112.5	120.5	120.5	120.5	122.5	126.5	129	131.5	133.5	133.5	
5.1	5.1	5 . 2	5.2	5.2	5.3	5.3	5.7	5.7	5.7	5. 8	6.0	6.1	6.2	6.3	6.3	
837	638	26926	918	6805	1557	1630	863	783	771	286	918	150	630	378	333	
ν	N	<b>,</b>	N	N	N	N	Ν	N	N	N	N	2	N	N	2	
A34898	A33991	I38344	· A44257	S20901	D41214	C41214	C38252	JH0329	B38252	S50039	A36337	в34631	I51086	S50040	S13684	
granulocyte colony	somatotropin recep	titin, cardiac mus	interleukin-6 sign	titin - rabbit (fr	protein-tyrosine-p	protein-tyrosine-p	granulocyte colony	granulocyte colony	granulocyte colony	granulocyte-macrop	membrane glycoprot	lactogen receptor	prolactin receptor	granulocyte-macrop	granulocyte-macrop	

## ALIGNMENTS

# RESULT

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A: RESIQUES: 333-420 <trav></trav>	A; Res
A; Molecule type: mRNA	A; Mol
A;Status: preliminary	A;Sta
A; Accession: A46175	A; Acc
A; Reference number: A46175; MUID:92357767; PMID:1495999	A; Ref
Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum	A;Tit
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992	Proc.
Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.	R; Tav
A; Experimental source: clone lambda h5R.25	A; Exp
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466	A;Cro
A;Residues: 1-332,'K' <mu3></mu3>	A; Res
A; Molecule type: mRNA	A; Mol
A;Accession: S21053	A; Acc
Experimental source: clone lambda h5R.27	A; Exp
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840	A;Cro
A; Residues: 1-395, 'I' <mu2></mu2>	A; Res
A; Molecule type: DNA	A; Mol
A;Accession: S21050	A; Acc
A; Experimental source: clone lambda h5R.12	A; Exp
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844	A;Cro
A; Residues: 1-420 <mur></mur>	A; Res
A; Molecule type: DNA	A; Mol
A;Accession: S21052	A; Acc
A; Reference number: S21050; MUID:92121815; PMID:1732409	A; Ref
A; Title: Molecular cloning and expression of the human interleukin 5 receptor.	A; Tit
J. Exp. Med. 175, 341-351, 1992	J. Ex
Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.	R;Mur
C; Accession: S21052; S21050; S21053; A46175; S78106; S78107	C; Acc
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000	C;Dat
C; Species: Homo sapiens (man)	C;Spe
terleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored	inter
1052	S21052
SULF 1	RESULT

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A; Accession. A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-426 <PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-13Ralpha 1 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: JC7773
R;Pierrot, C.; Beniguel, L.; Begue, A.; Khalife, J.
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                                                                                                                                                                                                                                                                            Local
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   KVESNYEHHNIQIMVKDNAGKIRPSYKIVSFTSNVKPGPPHIKHLFLKNGA--LFVQWKN
                                    EA-SDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP-VYLTFTRESSCEIKLKWSI 260
                                                                                  CKICHLWIKLFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
                                                                   LQCTWHNLSYMKCSWLPGKNTSPDTNYTLYYWYSSLGKSLQC-ENIHREGQHIGCSFKLT
                                                                                                                                -----KKELPLNEKICLOVGS----OCSTNESEKPSPLVKKC--ISPPRRG-SESAVTE 129
                                                                                                                                                              TKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWAETTYWISP--QGIPETKVQD 142
                                                                                                                                                                                             EVOPPVTNLSVSVENLCTIVMTWSPPEGAS -- PNCSLRYFSHFDDQQDKKIAPETRR---
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Pred.
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Pred. No. 4.6e-17;
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                                                                                                                                                                                                                                                                          296; DB 2;
No. 7.9e-16;
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C;Accession: JQ1655
R;Tanaka, M; Maeda, K; Okubo, T.; Nakashima, K.
B;Tanaka, M; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Blophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
                                                                                                                             prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
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A;Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; C;Keywords: cytokine receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, Cell 66, 1175-1184, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-5 receptor alpha chain precursor - human
c;Speciles: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C;Accession: A40267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-335 < TAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                           LGRNIACWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
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                                                   RSKVNIYCSDDGIWSEWS
                                                                                                                                    ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV
                                                                                                                                                                                                                                                                                                               THTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT
                                                                                                                                                                                                                                                                                                                                                                                                                   ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
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RAAVSSMCREAGLWSEWS
                                                                                                       EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                                                                                                                                                                         -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR
                                                                                                                                                                                                                                                                                                                                                                -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD
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28.0%;
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No. 1.2e-15;
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;439-462/Domain: transmembrane #status pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Takaki, S.; Tominaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; EMBO J. 9, 4367-4374, 1990
A;Title: Molecular cloning and expression of the murine interleukin-5 recepton A;Reference number: S12357; MUID:91092260; PMID:2265612
A;Accession: S12357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perleukin-5 receptor - mouse
species: Mus musculus (house mouse)
pecies: Mus musculus (house mouse)
pate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
paccession: S12357
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Best Local
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                                                           GFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
                                                                                                                                                                                                PPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLGVLSSLICLIMSWTMVLKGYRMITFMLP 473
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VTPLHEGFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVTNLTCTTHTVVSS
                                                                                                                                 PPVNFTIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES---
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                                                                                                                                                                                                                                                                                                  Score 247; DB 2;
Pred. No. 5.8e-12;
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Pred. No. 7.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 183; Indels
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                                                                                                                                                                                                                                                                      151;
                                                                                                                                                                                                                                                                                                                                  Length 415
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A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-369 <-RES>
A; Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
A; Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Wi
Hum. Mol. Genet. 2, 1099-1104, 1993
Hum. Mol. Genet. 2, 1099-1104, 1993
                                                                                             A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2;
A:Introns: associated with an X-linked for C:Superfamily: interleukin-2 receptor gamma chain C:Keywords: cytokine receptor; duplication; immunod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A42565; A46591; T54332
                                                                                                                                                                                                                                                                                                                                                                                                         Hum. Mol. Genet. 2, 1099-1104, 1993
A;Title: The interleukin-2 receptor gamma chain maps to A;Reference number: I54332; MUID:94004847; PMID:8401490
A;Accession: I54332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Takeshita, T.; Asao, F
Science 257, 379-382, 19
A; Title: Cloning of the
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                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-369 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A46591; MUID:93293887; A; Accession: A46591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J. J. Biol. Chem. 268, 13601-13608, 1993
A;Title: Characterization of the human interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: MOLT beta lymphoid cells
A; Note: sequence extracted from NCBI backbone (NCBIP:109167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Cloning of the gamma chain of the A; Reference number: A42565; MUID:92335883;
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                                                                                                                                                                                                                                                       A;Gene: GDB:IL2RG; SCIDX1; IMD4
                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L19546; NID:g349631; PIDN:AAC37524.1;
                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Noguchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D11086; NID:g303611; PIDN:BAA01857.1; PID:g219890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: nucleic acid; protein A;Residues: 1-369 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A42565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
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                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPLSAFPDHCFNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFINSKGFEQLAVHINGSSKRAAIKPFDQLFSPLAIDQVNPPRNVTVEIESN-SLYIQWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAVSSPCRMPGRWGEWS-QPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF--SLICR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPLGPIPARCEDYEIEIREDD------TTLVTATVENETYTLKTTNETRQLCFVV
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     Similarity
70; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, -382, 1992
                          10.5%;
Score 220; DB 2;
Pred. No. 6.9e-10;
8; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human IL-2 receptor
PMID:1631559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMID:8514792
                                                                                                immunodeficiency; severe
                                                                                                                                                 /2; 308/3
form of s
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                                                                                                                                                 severe combined
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                                                                                                                                                                                                                                                                                                      PID: g349632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma
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  36;
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Gaps
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97 LNKGIEAKIHTLLPWQCTNGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLC 155

·--PNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNC

19

LGVGLNTTILT --

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RESULT 7
I50455
interleukin-2
Cr&pecies: Mus
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F; 36-220/Domain: c
F; 240-426/Domain:
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A; Residues: 1-830 <CHE>
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C; Species: Columba livia (domestic
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                                                                                                       RESULT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     te: 13-Sep-1996 #sequence_revision
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                                                                                                                                                                                                  IKDMV-VWIIVGVLSSLICLV 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTNGSEVQSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTFGCTSSSDTEIKVNPPQDFEIVDPGYLG-----------YLYLQW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWNSSSEPQP----
                                                                                                                                                                                                                                                                 KKTLLREWLPFGFILILVIFV
                                                                                                                                                                                                                                                                                                                                                                                          TATVENETYTLKTTNETROLCFVV----RSKVNIYCSDD--GIWSEWS-DKQCWEGEDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTYIVQTDPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQNIVKPLPPVYLTFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPPLSLDHFKECTV-EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTYNITVMAMNEIGSNSS-----DPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAKW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHPIHW-GSNTSKEN-----PFLFALEAVVISVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SW------KPGIGVLLDTNYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
93; Conserv
      receptor gamma hous
                                                                                                                                                                                                                                                                                                                             -EEWETIFVGQQTHYKMFSLNPGKKYIVQIHCKPDHHGSWSEWSLEKYLQIPTDFR 436
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                                 chain
      mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 216.5; DB 2; Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pigeon)
sion 13-Sep-1996
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A;Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1 R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, Blochem. Blophys. Res. Commun. 193, 356-363, 1993 A;Title: Cloning of the mouse interleukin 2 receptor gamma A;Reference number: JN0592; MUID:93277575; PMID:8503926 A;Accession: JN0592
                                                                                                                                                                                                                                                                                                     A;Description: receptor for interleukin-2
A;Description: receptor for interleukin-1
A;Pathway: interleukin-2 stimulated growth and differentiation of T cell
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, Eur. J. Immunol. 24, 3014-3018, 1994
A;Title: The murine interleukin-2 receptor gamma chain gene: organ A;Reference number: I53398; MUID:95104285; PMID:7805729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A;Description: Regulation of CD44-mediated cellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 130, 303-304, 1993
A; Title: Cloning and sequencing of the cDNA encoding a PA; Reference number: JN0775; MUID:93366191; PMID:8359699
A; Accession: JN0775
  В
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                                                                                                                                                                                                                                F;1-22/Domain: signal sequence #status predicted <SIG>F;23-369/Product: interleukin-2 receptor gamma chain #sF;256-284/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns:
C; Complex:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-350, 'S', 352-366, 'S', 368-369
A; Cross-references: EMBL: X75337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S37582
A; Accession: S37582
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A;Residues: 1-369 <KOB>
A;Cross-references: GB.D13821; NID:g436045; PIDN:BAA02974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-369 <KUM>
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Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Tille: Characterization of cDNAs encoding the murine
                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                          eptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-369 < RES>
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A; Residues: 1-369 < RE2>
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A; Residues: 1-369 < CAO>
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C;Accession: 149280; A47514; JN0592; JN0775; S37582; I53398
                                                                                                                                                                                                     F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                        Matches
                                                  136 PETKVQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
53
                                                                                                                                Local Similarity
  PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 The high affinity receptor is a heterotrimer
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:S75852; NID:g861554; PIDN:AAB32904.1;
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                                                                                                                             10.1%;
26.9%;
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                                                                                                  43;
                                                                                                                                                                                                                                                        receptor gamma chain #status predicted
                                                                                                                          Score 212.5; DB 2
Pred. No. 2.7e-09;
                                                                                                     Mismatches
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o, H.; Nakamura, I
TNLTLHYRYKVSDNNTFQECSHYLF
                                                                                                                                                     DB 2;
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interleukin-2 receptor gamma chain precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: A55718
C;Accession: A55718
R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Fel
Genomics 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe A;Accession: A55718
A;Accession: A55718
A;Accession: A55718
A;Accession: A55718
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A; Residues: 1-373 <HEN>
A; Cross-references: GB:U04361; NID:g517411;
C; Superfamily: interleukin-2 receptor gamma
C; Keywords: cytokine receptor; duplication
                                                                  interleukin-3 receptor beta chain precursor - C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-C;Accession: A40091; A43022 R;Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman Science 247, 324-327, 1990
                                                                                                                                                                                RESULT 10
A40091
                                     A;Title: Cloning of an interleukin-3 receptor gene: a member A;Reference number: A40091; MUID:90117145; PMID:2404337
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                    A; Reference number: A40091; A; Accession: A40091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGSE-----VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL
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                                                                                                                                                                                                                                                                                                                           WDRSWTEQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCGSAQRWSEWSHPIHW-GSNTS
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                                                                                                                                                                                                                                                                                        KKTLL----RFWLPFGFILILVIFV
                                                                                                                                                                                                                                                                                                                                                            -DTTLVTATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLS
                                                                                                                                                                                                                                                                                                                                                                                                 --PRRQSTQKLKLQNLVIPWAPENLTLHNLSESQLELSWS---NRHLDHCLEHVVQYRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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     acid
   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
     not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 208; DB 2;
Pred. No. 6.3e-09;
8; Mismatches 108;
                                                                                                                                                                                                                                                        276
                                                                                                                                                                                                                                                                                          358
                                                                                                                            30-Jun-1993 #text_change
                                                                                         Gorman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: AAC48403.1;
                                                                                                                                                               mouse
                                                                                          D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                       Maruyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                       of
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                                                       Ø
                                                                                       K.; Ishii,
                                                                                                                            22-Jun-1999
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                                                       distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                     279
                                                                                         Α.;
                                                     receptor gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                          Yahara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 combine
A;Cross-references: GDB:126838; OMIM:138981
A;Map position: 22q13.1-22q13.1
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C;Keywords: alternative splicing; cytokine receptor; duplication; transmembra E;1-16/Domain: signal sequence #status predicted <SIG>
F;17-897/Product: cytokine receptor common beta chain #status predicted <MAT:
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A;Accesszon.
A;Accesszon.
A;Molecule type: mRNA
A;Residues: 1-815,'Q',817-878 <GOR>
A;Residues: 1-815,'Q',817-878 <GOR>
A:Cross-references: GB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
A:Cross-references: CB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Superfamily: interleukin-3 receptor beta chain; cytokine r c;Keywords: cytokine receptor; duplication; transmembrane pr F:1-22/Domain; signal sequence #status predicted <SIG> F:23-878/Product: interleukin-3 receptor beta chain #status
                                         A; Molecule type: mRNA
A; Residues: 1-897 <HAY>
A; Cross-references: GB:M38275
C; Comment: The human high-affinity
                                                                                                                                                                               R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor for human grand, Reference number: A39255; MUID:91088571; PMID:1702217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: A43022
A; Gene: GDB:CSF2RB
                                                                                                                                                                 A; Accession: A39255
                                                                                                                                                                                                                                                                                               C; Accession: A39255
                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Date: 30-Jun-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                          cytokine receptor common beta chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;463-878/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;441-462/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F; 254-433/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;39-236/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;23-440/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 PPQDFEIVDPGYLGYLYLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRVKPISDY - - - DGIWSEWSNEYTWT-TDWVMPTL- - - WI - - - - VLILVFLIFTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKLKWSIPLGPIPARCFD--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCFV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPQNLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPAAPEEKCSPVVKEPQASVYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKDGFDLNKGIEAKIHTLLP------WQCTNGSEVQ---SSWAETTYWISPQGIPET 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRSK-VNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSLHWETQKIP---KYIDHTFQVQYKKKSESWKDSKTENLGRVNSMDLPQLEPDTSYCAR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRCSLPVPEPSAHSQYTVSVKHLEQGKFI-MSYYHIQME-----PPILNQTKNRDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY-LTFTRESSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine receptor homology <CRS2> transmembrane #status predicted <TMM> intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%;
24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 195; DB 1
Pred. No. 2e-07;
                                                       IL-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                           30-Jun-1993 #text_change 02-Sep-1997
                                                       IL-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length
                                                       and
                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150;
                                                       GM-CSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460
                                                       have
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F:17-443/Domain: (F:35-232/Domain: (F:250-431/Domain: F:444-460/Domain: F:461-897/Domain:
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                                                                                                                                                                                                                                                                                                                                        A; Title: Cloning of rat interleukin-3 receptor beta-subunit A; Reference number: I56563; MUID:95370942; PMID:7643220 A; Accession: I56563
                                                                                                                                                                                                                                                                                                                                                                                R;Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, J. Neurosci. 15, 5800-5809, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-3 receptor beta-subunit -
                                                                                                                                                                                                       Superfamily: interleukin-3 receptor beta chain; cytokine | Keywords: cytokine receptor | 19-235/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                     ;Gene: rIL-3Rbeta
                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Rattus sp. (rat)
;Date: 26-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;250-431/Domain:
;444-460/Domain:
                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                         253-433/Domain: cytokine receptor homology <CRS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                               Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
                                                                                                                                                                                                                                                                                               atus: preliminary; translated
lecule type: mRNA
Residues: 1-896 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216
             152 LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                         50 YLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIH 106
                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                     IJ
                                                                                            VASSVSFGLFYKPSPDAGEEECSPVLR---EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPQSHWLSPGDLEFEVVYKRL-QDSWEDAAILLSNTS----QATLGPEHLMPSSTYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIPCOSEVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLVVPLAQHVQPPPPKDISISPSG--DHF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSEARSWDTESV-----LPMWVLALIVIFLTTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRKD----TATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGY---NGIWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IREDDTTLYTAT~VENETYTLKTTN------ETRQLCFV-VRSKVNIYCSDDGIWSE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KECTVEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKGIE------A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRAEKHIKSSV-----NI--QMAPPSLNVTKDGD-SYSLRWETMKMRYEHIDHTFEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE
                                                                                                                                    87; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular #status predicted <EXT>
cytokine receptor homology <CRS1>
cytokine receptor homology <CRS2>
transmembrane #status predicted <TMM>
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                8.5%;
21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 180.5; DB 1
22.6%; Pred. No. 2.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Mismatches 146;
                                                                                                                                                Score 178; DB 2;
Pred. No. 4.6e-06
                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                  Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             rat
                                                                                                                                                                                                                                                                                                                            GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
                                                                                                                                                            Length 896;
                                                                                                     -PPQDFEIVDPGYLGYL 49
                                                                                                                                                                                                                                                                                                                                                                                                 P.J
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                                                                                                                                  Indels
                                                                                                                                                                                                                                      receptor homology
                                                                                                                                                                                                                                                                                                                                                                  from cultured microglia
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                                                                                                                                  88;
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             203
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-896 <GORNA
A; Residues: 1-896 <GORN
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R;Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Ar Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like A;Reference number: A35782; MUID:90319131; PMID:1695379
A;Accession: A35782
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F;442-463/Domain: transmembrane #status predicted <TMM>
F;464-896/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;39-235/Domain: extracellular #status predicted <EXT>
F;39-235/Domain: cytokine receptor homology <CRS1>
VQYKKKSDSWEDSKTENLDRAHSMDLSQLEPDTSYCARVRVKPISNYDGIWSKWSEEYTW
                                                                                                                    IEIREDDTTLVTATVEN--ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCW 331
                                                                                                                                                                                                                                                V-----KHLEQGKFIMSYNHIQMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ
                                                                                                                                                                                                                                                                                                                                                                     VNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYAPRVRTRLYPGSSLSGR--PSRWSPEAHWDSQPG-DKAQPQNLQCFFDGIQSLHCSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEA-KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLLEWSVSLGDAQVSWLSSKDIEFEVAYKRL-QDSWEDAYSLHTSKFQVNFEPKLFLPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKN-----LHYKDGFDLNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVPRRCVIPY---TRFSITNEDYYSFRPDSDLGIQLMVPLAQNVQPPLPKNVSISSSEDR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLAIGCLYTFLISTTFGCTS-----SSDTEIK-----VNPPQDFEIVDPGYLGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNI----GCRFPYLEASDYKDFYIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWTQTTGSVSFGLFYRPSPVAPEEKCSPVVKEPPGASVYTRYHCSLPVPEPSAHSQYTVS
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Similarity 20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 173.5; DB 1;
Pred. No. 1e-05;
9; Mismatches 185;
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      437
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438 K-TDWVMPTL---WI----VLILVELILTLLL

363 461

EGEDLSKKTLLRFWLPFGFILILVIFVTGLLL

10;

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prolactin receptor Nb2 precursor - rat
(; Species: Rattus norvegicus (Norway rat)
(; Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
(; Accession: A41070; I55417
R; All, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A; Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant for A; Reference number: A41070; MUID:92041834; PMID:1718958
A; Accession: A41070
A; Molecule type: mRNA
A; Residues: 1-412 <ALI>A; Cross-references: GB:M74152; NID:9206389; PIDN:AAA41946.1; PID:9206390
R; O; Vesal K D; V
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-412 <RES>
A;Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964
A;Experimental source: Nb2-11C cell line
C;Superfamily: cytokine receptor homology
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A;Title: Cloning and expression of the rat prolactin receptor, a member of the A;Reference number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Accession: A29884
C;Accession: A29884
                                                                                                                                                                             R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short,
A;Reference number: 155417; MUID:95014432; PMID:7929319
A;Accession: 155417
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C;Keywords: transmembrane protein
F;1-19/Domain: signal sequence *status predicted <SIG>F;20-310/Product: prolactin receptor *status predicted F;31-216/Domain: cytokine receptor homology <CRS>
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esidues: 1-310 <BOU>
Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365
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l Similarity 28.5%; Pred. No. 1.3e-05;
63; Conservative 24; Mismatches 94;
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                                                                                                                                                                                                                 191 DGQNIGCRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLQNIVKPLPPVYLT 245
183 QTQFKVFDLYPGQKYLVQTRCK---PDHGYWSRWSQESSVE 220
                                                                                                                             246 F----TRESSCEIKLKWSIP-LGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
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